



SEQUENCE LISTING

<110> DAI, KEN-SHWO
<120> HUMAN ARL-RELATED GENE VARIANTS ASSOCIATED WITH CANCER
<130> U014798-3
<140> 10/653,681
<141> 2003-09-02
<160> 4
<170> PatentIn version 3.2
<210> 1
<211> 1090
<212> DNA
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<223> VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

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<222> (70)..(333)

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Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro
1 5 10

att gtg ggc ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa 159
Ile Val Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu
15 20 25 30

gca gtg aag gtg gcc att gat gca gga tat cgg cac att gac tgt gcc 207
Ala Val Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala
35 40 45

tat gtc tat cag aat gaa cat gaa gtg ggg gaa gcc atc caa gag aag 255
Tyr Val Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys
50 55 60

atc caa gag aag gct gtg aag cgg gag gac ctg ttc atc gtc agc aag 303
Ile Gln Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys
65 70 75

ttg tgg ccc act tcc aga tcg aga agc tct tgaacaaacc tggactgaaa 353
Leu Trp Pro Thr Ser Arg Ser Arg Ser Ser
80 85

tataaaccag tgactaacca ggttgagtgt cacccatacc tcacgcagga gaaactgatc 413
cagtaactgcc actccaaggg catcacccgtt acggccatac gccccctggg ctctccggat 473
agacaccttggg ccaagccaga agacccttcc ctgctggagg atcccaagat taaggagatt 533

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gactttaaat tgagtgtatga ggagatggca accatactca gcttcaacag aaactggagg	713
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Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val
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Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val
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Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln
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Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp
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Pro Thr Ser Arg Ser Arg Ser Ser
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<223> VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

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Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro
1 5 10

att gtg ggc ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa 159
Ile Val Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu
15 20 25 30

gca gtg aag gtg gcc att gat gca gga tat cgg cac att gac tgt gcc 207
Ala Val Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala
35 40 45

tat gtc tat cag aat gaa cat gaa gtg ggg gaa gcc atc caa gag aag 255
Tyr Val Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys
50 55 60

atc caa gag aag gct gtg aag cgg gag gac ctg ttc atc gtc agc aag 303
Ile Gln Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys
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Lys Thr Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile
95 100 105 110

cac tgg cca cag gga ttc aag tct ggg gat gac ctt ttc ccc aaa gat 447
His Trp Pro Gln Gly Phe Lys Ser Gly Asp Asp Leu Phe Pro Lys Asp
115 120 125

gat aaa ggt aat gcc atc ggt gga aaa gca acg ttc ttg gat gcc tgg 495
Asp Lys Gly Asn Ala Ile Gly Gly Lys Ala Thr Phe Leu Asp Ala Trp
130 135 140

gag gcc atg gag gag ctg gtg gat gag ggg ctg gtg aaa gcc ctt ggg 543
Glu Ala Met Glu Glu Leu Val Asp Glu Gly Leu Val Lys Ala Leu Gly
145 150 155

gtc tcc aat ttc agc cac ttc cag atc gag aag ctc ttg aac aaa cct 591
Val Ser Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro
160 165 170

gga ctg aaa tat aaa cca gtg act aac cag gtt gag tgt cac cca tac 639
Gly Leu Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr
175 180 185 190

ctc acg cag gag aaa ctg atc cag tac tgc cac tcc aag ggc atc acc	687
Leu Thr Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr	
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gtt acg gcc tac agc ccc ctg ggc tct ccg gat aga cct tgg gcc aag	735
Val Thr Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys	
210 215 220	
cca gaa gac cct tcc ctg ctg gag gat ccc aag att aag gag att gct	783
Pro Glu Asp Pro Ser Leu Leu Glu Asp Pro Lys Ile Lys Glu Ile Ala	
225 230 235	
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Ala Lys His Ser Pro Ser Leu	
240 245	
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aatatttggg ttgaatctcc tggtagatt atacaggaga ttcttttct tcgctgaagt	1014
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Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro Ile Val
 1 5 10 15

Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val
 20 25 30

Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val
 35 40 45

Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln
 50 55 60

Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp

65

70

75

80

Pro Thr Phe Phe Glu Arg Pro Leu Val Arg Lys Ala Phe Glu Lys Thr
85 90 95

Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile His Trp
100 105 110

Pro Gln Gly Phe Lys Ser Gly Asp Asp Leu Phe Pro Lys Asp Asp Lys
115 120 125

Gly Asn Ala Ile Gly Gly Lys Ala Thr Phe Leu Asp Ala Trp Glu Ala
130 135 140

Met Glu Glu Leu Val Asp Glu Gly Leu Val Lys Ala Leu Gly Val Ser
145 150 155 160

Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro Gly Leu
165 170 175

Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr Leu Thr
180 185 190

Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr Val Thr
195 200 205

Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys Pro Glu
210 215 220

Asp Pro Ser Leu Leu Glu Asp Pro Lys Ile Lys Glu Ile Ala Ala Lys
225 230 235 240

His Ser Pro Ser Leu
245